```
                                                    Cys-rich
       FcRY:  MLGVLLLACCLLLGGRSLPRG DAALSRDELPSLRNKGIFIIQSSGSNL   25
human PLA2R: MLLSPSLLLLLLLGGAAGCAEGVAALTPERLLEWQDKGIFVIQSESLKK   25
   human MR:        MRLPLLLVFASVIPG  AVL    LLDTRQ   FLIYNEDHKR   16
  Consensus: -----------LL--------G--A-L----L--------F-I-------

       FcRY: CIKADTAGLVLEDCS  QISKHMLWKWVSNRRLFNIGRSSCLGLNISRPE   73
human PLA2R: CIQAGKSVLTLGRTGSKQANKHMLWKWVSNHGLFNIGGSGCLGLNFSAPE   75
   human MR: CVDA VSPSAVQTAACNQDAESQKFRWVSESQIMSVAFKLCLGVPSKTDW   65
  Consensus: C--A-------------Q--------WVS-----------CLG-------

       FcRY: QPLTMLECDSNRYSLWWNCDGRALVGV    SEYRLAVENSKRIVAKKKS   119
human PLA2R: QPLSLYECDSTLVSLRWRCNRKMITGP    LQYSVQVAHDNTVVASRKY   121
   human MR: VAITLYACDSKSEFQKWECKNDTLLGIKGEDLFFNYGNRQEKNIMLYKGS   115
  Consensus: -------CDS------W-C------G-----------------------

                                FNII
       FcRY: DY  QWIQYMSYDEDLCEHPFQETYTLLGNSFGFPCVFPFKYNNKWYYEC   167
human PLA2R: IH  KWISYGSGGGDICEYLHKDLHTIKGNTHGMPCMFPFQYNHQWHHEC   169
   human MR: GLWSRWKIYGTTD NLCSRGYEAMYTLLGNANGATCAFPFKFENKWYADC   164
  Consensus: -----W--Y-------C--------T--GN--G--C-FPF-----W---C

                                            CTLD1
       FcRY: TRDGKEFE  WCATTSYYEQDEKWGFCPG   VEHGCGTFWKENPATHVC   212
human PLA2R: TREGREDDLLWCATTSRYERDEKWGFCPDPTSAEVGCDTIWEKDLNSHIC   219
   human MR: TSAGRSDGWLWCGTTTDYDTDKLFGYCP  LKFE GSESLWNKDPLTSVS   211
  Consensus: T--G------WC-TT--Y--D---G-CP-----E-G----W---------

       FcRY: YQFNPSAVLSWHEARAACQAQGGDLLSITSPEEQSYLSNLSRQLNTTDAV   262
human PLA2R: YQFNLLSSLSWSEAHSSCQMQGGTLLSITDETEENFIRE   HMSSKTVE   266
   human MR: YQINSKSALTWHQARKSCQQQNAELLSITEIHEQTYLTGLT   SSLTSG   258
  Consensus: YQ-N----L-W--A---CQ-Q---LLSIT---E----------------

       FcRY: LWTGLNRLEEGAGWQWSDGAPLVFVNWKADVSEDHSSENHCAVMSSKLKY   312
human PLA2R: VWVGLNQLDEDAGWQWSDGTPLNYLNWSPEVNFEPFVEDHCGTFSSFMPS   316
   human MR: LWIGLNSLSFNSGWQWSDRSPFRYLNWLPG SPSAEPGKSCVSLNPGKNA   307
  Consensus: -W-GLN-L----GWQWSD--P----NW------------C---------
```

CTLD2

```
       FcRY: GWKSYLCESGLPFVCKKYLNKIEQETL  DTWKYYATRCDAGWYPYNRYC   360
human PLA2R: AWRSRDCESTLPYICKKYLNHIDHEIVEKDAWKYYATHCEPGWNPYNRNC   366
   human MR: KWENLECVQKLGYICKKGNTTLNSFVIPSESD  VPTHCPSQWWPYAGHC   355
  Consensus: -W----C---L---CKK------------------T-C---W-PY---C

       FcRY: YRLHKEAKSWN DALISCQSDSSGLISISSMADAELLHNLLQRENITETW   409
human PLA2R: YKLQKEEKTWH EALRSCQADNSALIDITSLAEVEFLVTLLGDENASETW   415
   human MR: YKIHRDEKKIQRDALTTCRKEGGDLTSIHTIEELDFIISQLGYEPNDELW   405
  Consensus: Y------K-----AL--C------L--I-----------L--E---E-W

       FcRY: IGLYNSNISVVFEWSDGTPVKFSYWHSQEPNTFQRAGQLCVSAQGPEGHW   459
human PLA2R: IGLSSNKIPVSFEWSNDSSVIFTNWHTLEPHIFPNRSQLCVSAEQSEGHW   465
   human MR: IGLNDIKIQMYFEWSDGTPVTFTKWLRGEPSHENNRQEDCVVMKGKDGYW   455
  Consensus: IGL----I---FEWS----V-F--W---EP---------CV------G-W
```

CTLD3

```
       FcRY: KVKKCEDKNFYICK KAGEFNSVSSDAESSCPEGWERHGGYCYKIDSTPR   508
human PLA2R: KVKNCEERLFYICK KAGH   VLSDAESGCQEGWEETCGFCYKIDTVLR   511
   human MR: ADRGCEWPLGYICKMKSRSQGPEIVEVEKGCRKGWKKHHFYCYMIGHTLS   505
  Consensus: ----CE----YICK-K-----------E--C--GW------CY-I-----

       FcRY: SFEHASSGYFCPSA LVSVTNRFEQAFITSMIRSVVKSERTYFWIGLQDL   557
human PLA2R: SFDQASSGYYCPPA LVTITNRFEQAFITSLISSVVKMKDSYFWIALQDQ   560
   human MR: TFAEANQTCNNENAYLTTIEDRYEQAFLTSFVG  LRPEK YFWTGLSDI   552
  Consensus: -F--A--------A-L-----R-EQAF-TS-----------YFW--L-D-

       FcRY: NNTGEYVWLTKDGKNHSVSYTNWNKHQPRHSGGCVAMRGQDPVGYWEVKS   607
human PLA2R: NDTGEYTWKPVGQKPEPVQYTHWNTHQPRYSGGCVAMRGRHPLGRWEVKH   610
   human MR: QTKGTFQW TIEEE   VRFTHWNSDMPGRKPGCVAMRTGIAGGLWDVLK   598
  Consensus: ---G---W---------V--T-WN---P----GCVAMR-----G-W-V--
```

CTLD4

```
       FcRY: CKNFKAMSLCKQKISSYEEPELTFQRHLSSCYFGWESEGNLLNCYKIFHR   657
human PLA2R: CRHFKAMSLCKQPVENQEKAEYEERWPFHPCYLDWESEPGLASCFKVFHS   660
   human MR: CDE KAKFVCKHWAEGVTHPPKPTTTPEPKCPEDWGASSRTSLCFKLYAK   647
  Consensus: C---KA---CK------------------C---W--------C-K----

       FcRY: EKILMKRTWSEAETLCQDFGAHLASFSHVYEETFLNNLLYTIFDRTEERQ   707
human PLA2R: EKVLMKRTWREAEAFCEEFGAHLASFAHIEEENFVNELLHPKFNWTEERQ   710
   human MR: GKHE KKTWFESRDFCRALGGDLASINNKEEQQTIWRLITA  SGSYHKL   694
  Consensus: -K---K-TW-E----C---G--LAS-----E------L------------

       FcRY: FWIGFNRRNPFSGGTWQWSDRTPVVASFLESKYVE DDSRN   CGVFKV   753
human PLA2R: FWIGFNKRNPLNAGSWEWSDRTPVVSSFLDNTYFG EDARN   CAVYKP   756
   human MR: FWLGLTYGSP SEG FTWSDGSPV  SYENWAYGEPNNYQNVEYCGELKG   740
  Consensus: FW-G-----P---G---WSD--PV--S-----Y-------N---C---K-
```

CTLD5

```
       FcRY: NRTIF  PAHCNEKREWICKIPKGVKPK NPDWYIAELP      WSYYQ   794
human PLA2R: NKTLL  PLHCGSKREWICKIPRDVKPK IPFWYQYDVP      WLFYQ   797
   human MR: DPTMSWNDINCEHLNNWICQIQKGQTPKPEPTPAPQDNPPVTEDGWVIYK   790
  Consensus: --T-------C-----WIC-I-----PK--P-------P------W--Y-

       FcRY: GAEYLFHVNPTDWDTYEFICVWLRSEMATIHSADEQAFIENKIKKLSDSD   844
human PLA2R: DAEYLFHTFASEWLNFEFVCSWLHSDLLTIHSAHEQEFIHSKIKALSKYG   847
   human MR: DYQYYFSKEKETMDNARAFCKRNFGDLVSIQSESEKKFLWKYVNR NDAQ   839
  Consensus: ---Y-F------------C---------I-S--E--F------------

       FcRY: VHWWIGLHAESISNEFRWKDGSQITYQNWNEGRDRYLRKPGKRCGFISSQ   894
human PLA2R: ASWWIGLQEERANDEFRWRDGTPVIYQNWDTGRERTVNNQSQRCGFISSI   897
   human MR: SAYFIGLLI SLDKKFAWMDGSKVDYVSWATG EPNFANEDENCVTMYSN   887
  Consensus: ----IGL--------F-W-DG----Y--W--G-----------C----S-
```

CTLD6

```
       FcRY: TGRWDDENCTVSLPCICKR KSAWKIEKEIPKDQNPQGTCPKGWLHFGYK   943
human PLA2R: TGLWGSEECSVSMPSICKR KKVWLIEKKKDTPKQ HGTCPKGWLYFNYK   945
   human MR: SGFWNDINCGYPNAFICQRHNSSINATTVMPTMPSVPSGCKEGWNFYSNK   937
  Consensus: -G-W----C------IC-R--------------------C--GW-----K

       FcRY: CFLIQIPKDPEHLRSWYSAQTFCSRYDGSLASLEDELEQAFITMNLFGRK    993
human PLA2R: CLLLNIPKDPSSWKNWTHAQHFCAEEGGTLVAIESEVEQAFITMNLFGQT    995
   human MR: CFKI FGFMEEERKNWQEARKACIGFGGNLVSIQNEKEQAFLTYHMKDST    986
  Consensus: C--------------W--A---C----G-L-----E-EQAF-T-------

       FcRY: TSVWIAFQGDDYEK   WMNENPPRYSNWSPIEAVHRPRYNGVYVEEQVP   1040
human PLA2R: TSVWIGLQNDDYET   WLNGKPVVYSNWSPFDIINIPSHNTTEVQKHIP   1042
   human MR: FSAWTGLNDVNSEHTFLWTDGRGVHYTNWG  KGYPGGRRSSLSYEDAD   1033
  Consensus: -S-W--------E----W-------Y-NW--------------------
```

CTLD7

```
       FcRY: LCTLVSNNPNFYFTGKWYLENCEKN YGFVCQKGQDTSRHIVNASEMYPV   1089
human PLA2R: LCALLSSNPNFHFTGKWYFEDCGKEGYGFVCEKMQDTSGHGVNTSDMYPM   1092
   human MR:  CVVIIGGASNE AGKWMDDTCDSKR GYICQTRSDPS  LTNPPATIQT   1078
  Consensus: -C------------GKW----C-----G--C----D-S----N-------

       FcRY: PDTLQYANRTYTLIRGNFTWSAALKACMANGAELVSIADQYHQSFLTIIV   1139
human PLA2R: PNTLEYGNRTYKIINANMTWYAAIKTCLMHKAQLVSITDQYHQSFLTVVL   1142
   human MR: DGFVKYGKSSYSLMRQKFQWHEAETYCKLHNSLIASILDPYSNAFAWLQM   1128
  Consensus: -----Y----Y--------W--A---C--------SI-D-Y---F-----

       FcRY: NRLGYNHWIGLFTADNGLNFEWSDGTRSLFTFWEDDESQALGSCVYMDTS   1189
human PLA2R: NRLGYAHWIGLFTTDNGLNFDWSDGTKSSFTFWKDEESSLLGDCVFADSN   1192
   human MR: ETSNERVWIALNSNLTDNQYTWTDKWRVRYTNWAADEPKLKSACVYLDLD   1178
  Consensus: -------WI-L----------W-D------T-W---E------CV--D--
```

CTLD8

```
       FcRY: GRWKSTSCERLLPGAVCHVPPKKKLTEYKGL   CSESN VPWIKFKNSC   1235
human PLA2R: GRWHSTACDSFLQGAICHVPPETRQSEHPEL   CSETS IPWIKFKSNC   1238
   human MR: GYWKTAHCNESFY FLCKRSDEIPATEPPQLPGRCPESDHTAWIPFHGHC   1227
  Consensus: G-W----C--------C---------E---L---C-E-----WI-F---C

       FcRY: YSFNTVLQGTSFDTAYEVCRNQGSNLLTIKDEDENAFILEELHSFGYSVK   1285
human PLA2R: YKFSTVLDSMSFEAAHEFCKKEGSNLLTIKDEAENAFLLEELFAFGSSVQ   1288
   human MR: YYIESSYTRNWGQASLE CLRMGSSLVSIESAAESSFLSYRVEPLKSKTN   1276
  Consensus: Y---------------E-C---GS-L--I----E--F-------------

       FcRY: MVWLNILQVTDNETVSWFDGSPLNYSNWGIREPEFDHLKGNFCISLRTAD   1335
human PLA2R: MVWLNAQFDGNNETIKWFDGTPTDQSNWGIRKPDTDYFKPHHCVALRIPE   1338
   human MR: F WIGLFRNVEG TWLWINNSPVSFVNWNTGDPSGER   NDCVALHASS   1321
  Consensus: --W----------T--W----P----NW----P---------C--L----

                                                          TM
       FcRY: GVWQISPCREIKGFVCKK    DA    DLDAAEP SKK    QSYPGLA   1372
human PLA2R: GLWQLSPCQEKKGFICKM    EA    DIHTAEALPEK    GPSHSII   1376
   human MR: GFWSNIHCSSYKGYICKRPKIIDAKPTHELLTTKADTRKMDPSKPSSNVA   1371
  Consensus: G-W----C---KG--CK------A--------------K-----------

                                  Cytoplasmic ØxNxxY
       FcRY: ALAVFVTLVMLAAISFFLWCLYKQNNRFFHRILWVRNAYFPQINSDAPAL   1422
human PLA2R: PLAVVLTLIVIVAICTLSFCIYKHNGGFFRRLAGFRNPYYPATNFSTVYL   1426
   human MR: GVVIIVILLILTGAGLAAYFFYKKRRVHLPQEGAFENTLYFNSQSSPGTS   1421
  Consensus: -------L-------------YK-------------N-------------

             ExxxØØ
       FcRY: EESILISDFERDDN                                      1436
human PLA2R: EENILISDLEKSDQ                                      1440
   human MR: DMKDLVGNIEQNEHSVI                                   1438
  Consensus: ----L----E-------
```